

Applying MESA Epidemiological Model to Human Diseases



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Although existing human epidemiological models are highly sophisticated and useful, they do not have the capability to assess the full distribution of epidemiological impacts from diseases since many of them are fixed point estimate input/output models. This study applies the Multi-Scale Epidemiologic Simulation and Analysis (MESA) system used for foreign animal diseases to assess consequences from a human disease outbreak in the United States.

The advantageous computational capabilities of the MESA system enable a broad array of extensive stochastic analyses of model runs. The methodology applied here divides census tract level data into different demographics. Analysis of a baseline influenza scenario indicated that one of the following outcomes will result: 1) the outbreak burns itself out before it has a chance to spread regionally; 2) the outbreak spreads regionally and lasts a relatively long time; or 3) the outbreak spreads through air travel and lasts a long time with unconstrained geography becoming a nationwide pandemic. These results are similar to historical trends in real-world influenza outbreaks.

Project Goals

The goal of this project was to apply the existing MESA model to human influenza and evaluate its capability to provide stochastic analysis output for a fixed set of input parameters. Relevant modeling literature was reviewed and components necessary for a nationwide epidemiological model were identified. Next, the MESA modeling approach was assessed and relevant databases on population, mixing behavior, and disease spread needed to instantiate the model were identified and gathered. Finally, the MESA model was applied by loading the relevant databases and assessing output.

Relevance to LLNL Mission

There is a need for an accurate and computationally efficient human epidemiological simulation model that incorporates detection events and countermeasures in a meaningful way. The model created in this study improves LLNL's competency in human epidemiology, which will help identify requirements for biological detection and countermeasure strategies to address this

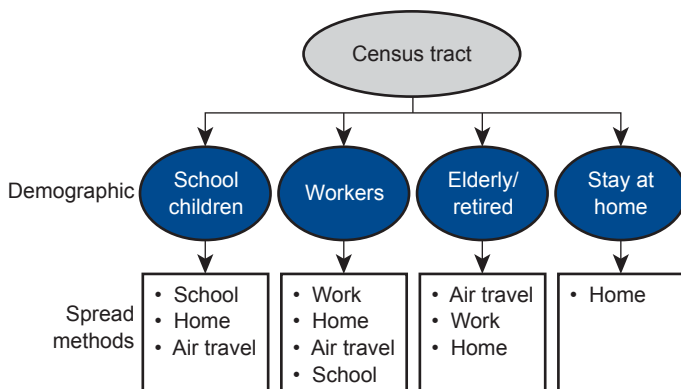


Figure 1. Breakdown of census tracts into four demographic variables and associated spread methods used for modeling human populations and disease spread using the MESA model.

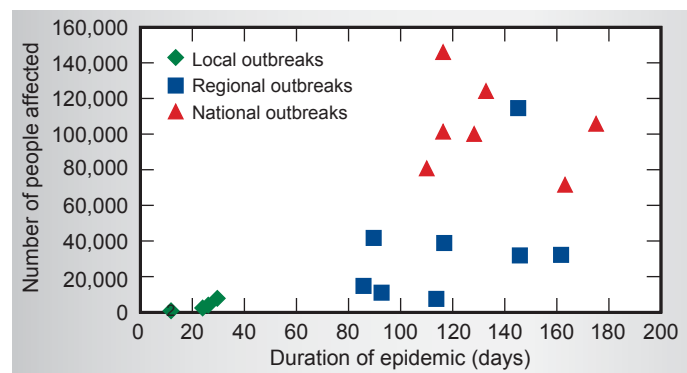


Figure 2. Number of people affected by the duration of the outbreak for 20 baseline scenario model runs.

threat. This capability will improve the Laboratory's planning and response capabilities for biological threats through improved inference and prediction.

FY2008 Accomplishments and Results

Different demographics in human populations are comparable to different herd types in the animal model. Therefore, US Census data at the census tract level were broken down into four overarching demographics (Fig. 1), including school aged children, work-force adults, retired/elderly persons, and stay-at-home individuals.

There are two spread models in MESA. The intra-facility model contains a basic SEIR model populated with influenza parameters used to simulate spread within a census tract and a specific demographic group. The inter-facility spread model is an agent-based model, which contains four different spread methods: schools, workplaces,

households, and air travel. The air travel spread method was populated with airport boarding statistics for major airports, which enabled a gravitational model to probabilistically assign air traveler destinations.

To simulate a baseline scenario, an index case of an infected school child was placed in Queens, New York, and simple social distancing control measures were implemented after disease detection occurs. These control measures restricted school- and work-related contacts after disease confirmation and ultimately restricted air travel of infected persons. Twenty instances of the baseline scenario are shown in Fig. 2.

Outbreaks fell into one of three categories: those that spread locally, those that spread regionally, and those that spread nationally. Figure 3 displays the geographic extent of spread for each type of outbreak. Among local outbreaks, the disease burned itself out on its own. Among regional outbreaks, the disease

adversely affected school children near the index case, but eventually control measures contained disease spread. Among national outbreaks, airline passengers enabled the disease to spread unnoticed far beyond the state of introduction.

These results conform to CDC historical influenza data which show that the majority of influenza outbreaks are limited to local or regional outbreaks, but periodically a pandemic occurs if it spreads further and faster than control measures can monitor and contain it. The study has shown that scaling up regional models is not effective because of a wide range of complex variables that must be accounted for in a nationwide epidemic.

Related References

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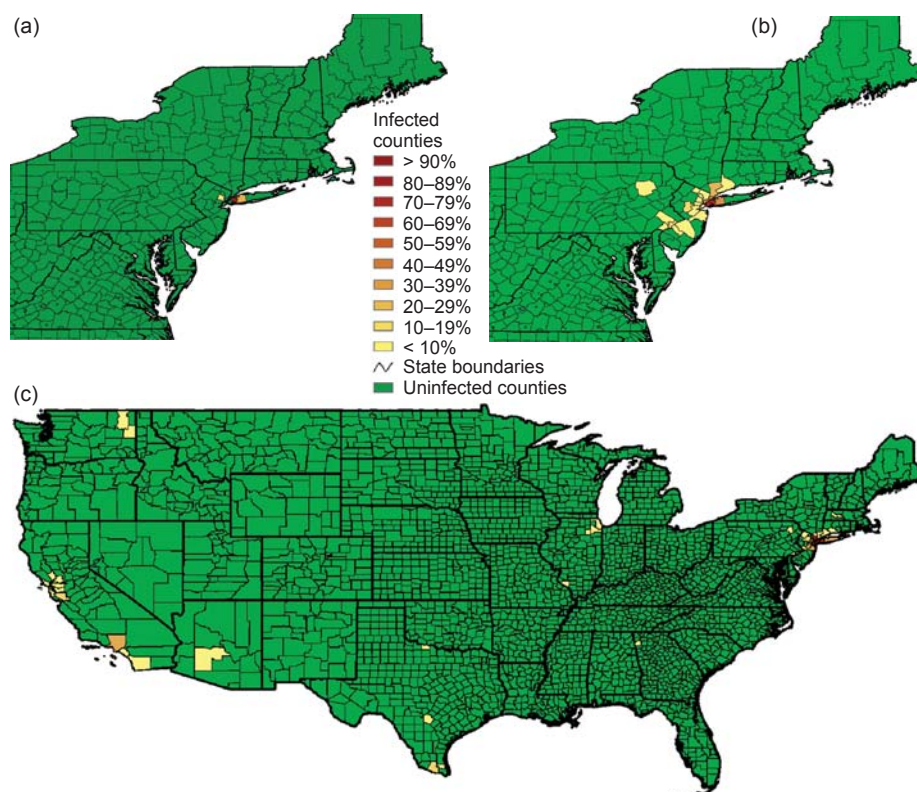


Figure 3. Geographic spread of each class of simulated outbreaks from the MESA model for (a) local outbreaks, (b) regional outbreaks, and (c) national outbreaks.